GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:06:55 ; Search time 755.06 Seconds
(without alignments)
27.251 Million cell updates/sec

Title: US-09-851-670-3
Perfect score: 24
Sequence: 1 tggctggtctgggatgtcggaagg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	16.2	67.5	55	14	AAQ41951	Ig alpha1 CH1 regi
c	2	16.2	67.5	55	14	AAQ41952	Ig alpha2 CH1 regi
c	3	16.2	67.5	60	19	AAV21370	Immunoglobin genom
c	4	15	62.5	30	19	AAT99618	Protein kinase LIM
c	5	14.6	60.8	40	17	AAT70675	Fibrin clot bindin
c	6	14.4	60.0	33	20	AAZ25247	Plasmid constructi
	7	14.4	60.0	33	20	AAZ25248	Plasmid constructi
c	8	14.4	60.0	43	19	AAV00317	Bacillus thuringie
c	9	14.4	60.0	43	22	AAF73235	Oligonucleotide #2
c	10	14.2	59.2	31	21	AAZ49486	PCR primer XDH2UP-
c	11	14	58.3	20	14	AAQ49692	PKC-gamma translat
c	12	14	58.3	20	16	AAQ97909	PNA oligomer targe
c	13	14	58.3	20	16	AAQ84196	PKC-gamma antisens
c	14	14	58.3	20	19	AAV35536	Oligo ON36 targete
c	15	14	58.3	20	20	AAZ27301	Human protein kina
c	16	14	58.3	20	20	AAX78559	Human PKC-gamma ol
c	17	14	58.3	20	20	AAX83668	Human protein kina
c	18	14	58.3	20	20	AAX22597	Human protein kina
c	19	14	58.3	20	20	AAX19162	Human PKC-gamma an
	20	14	58.3	24	22	AAC87564	TGAT SECIS element
	21	14	58.3	29	20	AAX28666	Nucleotide sequenc
	22	14	58.3	29	21	AAF00326	Hammerhead ribozym
	23	14	58.3	60	16	AAT00238	Thrombin 60N DNA l
	24	14	58.3	60	22	AAF70790	Thrombin high affi
	25	13.8	57.5	30	22	AAF44559	Mouse DSS-induced
	26	13.6	56.7	20	20	AAX81591	PCR primer used to
	27	13.6	56.7	26	20	AAX57350	PArvovirus detecti
c	28	13.6	56.7	27	22	AAC86683	DNA encoding a hae
c	29	13.6	56.7	30	21	AAZ49882	Oligonucleotide fo
c	30	13.6	56.7	33	19	AAV07684	Influenza haemaggl
	31	13.6	56.7	42	20	AAX76869	PCR primer for clo
c	32	13.6	56.7	43	16	AAQ80044	Primer #1 for epit
	33	13.6	56.7	43	18	AAT91996	Primer for human c
c	34	13.6	56.7	43	18	AAT43254	Human glutathione
	35	13.6	56.7	45	16	AAQ80045	Primer #2 for epit
	36	13.6	56.7	45	18	AAT43255	Human glutathione
c	37	13.6	56.7	45	20	AAX76870	PCR primer for clo
	38	13.6	56.7	47	19	AAV23663	Human interleukin-
c	39	13.6	56.7	48	20	AAV72975	Human Doc2-alpha P
	40	13.6	56.7	48	20	AAV72976	Human Doc2-alpha P
	41	13.6	56.7	49	17	AAT13006	Adrenergic recepto
	42	13.6	56.7	50	19	AAV34690	Yeast YCF1 gene re
c	43	13.6	56.7	51	16	AAQ88791	Influenza HA epito
	44	13.6	56.7	51	18	AAT88963	3' PCR primer used
	45	13.6	56.7	51	20	AAX02168	Human h4-1BBSV rec

ALIGNMENTS

RESULT 1
AAQ41951/c
ID AAQ41951 standard; DNA; 55 BP.
XX
AC AAQ41951;
XX
DT 08-SEP-1993 (first entry)
XX
DE Ig alpha1 CH1 region intron/exon sequence flanking 3' splice site.
XX
KW Antisense oligonucleotide; immunoglobulin; pre-mRNA splicing;
KW intron removal; antibody production; transcriptional regulation;
KW allergy; immunosuppression; heavy chain; constant region; CH1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 1
FT /*tag= a
FT /note= "conserved branch point residue"
FT misc_feature 34..35
FT /*tag= b
FT /note= "3' intron-exon junction"
FT misc_feature 1..35
FT /*tag= c
FT /note= "Pref. oligonucleotides of the invention are
FT complementary to at least a continuous 12nt
FT sequence from this region or with a portion
FT of this segment and a continuous portion of
FT the sequence downstream of the splice site"
XX
PN WO9310138-A.
XX
PD 27-MAY-1993.

```
XX
PF   18-NOV-1992;   92WO-US10024.
XX
PR   18-NOV-1991;   91US-0794395.
XX
PA   (TANO-) TANOX BIOSYSTEMS INC.
XX
PI   Chang TW;
XX
DR   WPI; 1993-182481/22.
XX
PT   Anti-sense oligo-nucleotide(s) for isotype-specific suppression
PT   of immunoglobulin prodn. - used for treating auto-immune diseases
PT   and allergies and causing humoral immunosuppression
XX
PS   Claim 7; Page 22; 32pp; English.
XX
CC   Oligonucleotides complementary to the splicing recognition region
CC   of Ig pre-mRNA are preferably complementary to at least a continuous
CC   12 nucleotide sequence of the region indicated in the features table.
CC   Such antisense oligonucleotides can be used to prevent or inhibit
CC   maturation of Ig mRNA and hence interfere with production of
CC   funtional immunoglobulins. Selective suppression of Ig isotypes can
CC   be used to cause humoral immunosuppression for treating allergies
CC   and autoimmune diseases.
XX
SQ   Sequence 55 BP; 10 A; 22 C; 13 G; 10 T; 0 other;


  Query Match             67.5%;  Score 16.2;  DB 14;  Length 55;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 ggctggtctgggatgtcggaa 22
           |||||||| ||||||  ||||
Db      50 GGCTGGTCGGGGATGCTGGAA 30


RESULT   2
AAQ41952/c
ID   AAQ41952 standard; DNA; 55 BP.
XX
AC   AAQ41952;
XX
DT   08-SEP-1993  (first entry)
XX
DE   Ig alpha2 CH1 region intron/exon sequence flanking 3' splice site.
XX
KW   Antisense oligonucleotide; immunoglobulin; pre-mRNA splicing;
KW   intron removal; antibody production; transcriptional regulation;
KW   allergy; immunosuppression; heavy chain; constant region; CH1; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "conserved branch point residue"
FT   misc_feature    34..35
FT                   /*tag=  b
FT                   /note= "3' intron-exon junction"
FT   misc_feature    1..35
FT                   /*tag=  c
FT                   /note= "Pref. oligonucleotides of the invention are
FT                          complementary to at least a continuous 12nt
FT                          sequence from this region or with a portion
FT                          of this segment and a continuous portion of
FT                          the sequence downstream of the splice site"
XX
PN   WO9310138-A.
XX
PD   27-MAY-1993.
XX
PF   18-NOV-1992;   92WO-US10024.
XX
PR   18-NOV-1991;   91US-0794395.
XX
PA   (TANO-) TANOX BIOSYSTEMS INC.
XX
PI   Chang TW;
XX
DR   WPI; 1993-182481/22.
XX
PT   Anti-sense oligo-nucleotide(s) for isotype-specific suppression
PT   of immunoglobulin prodn. - used for treating auto-immune diseases
PT   and allergies and causing humoral immunosuppression
XX
PS   Claim 7; Page 22; 32pp; English.
XX
CC   Oligonucleotides complementary to the splicing recognition region
CC   of Ig pre-mRNA are preferably complementary to at least a continuous
CC   12 nucleotide sequence of the region indicated in the features table.
CC   Such antisense oligonucleotides can be used to prevent or inhibit
CC   maturation of Ig mRNA and hence interfere with production of
CC   funtional immunoglobulins. Selective suppression of Ig isotypes can
CC   be used to cause humoral immunosuppression for treating allergies
CC   and autoimmune diseases.
XX
SQ   Sequence 55 BP; 10 A; 23 C; 13 G; 9 T; 0 other;


  Query Match             67.5%;  Score 16.2;  DB 14;  Length 55;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 ggctggtctgggatgtcggaa 22
           |||||||| ||||||  ||||
Db      50 GGCTGGTCGGGGATGCTGGAA 30


RESULT   3
AAV21370/c
ID   AAV21370 standard; DNA; 60 BP.
XX
AC   AAV21370;
XX
DT   14-AUG-1998  (first entry)
XX
DE   Immunoglobin genomic CH alpha 1.
XX
KW   ss; Ig; heavy chain; stimulation; inhibition; treatment; IgM; IgG; IgA;
KW   IgE; isotype switching; allergy; autoimmune; alloimmune.
XX
OS   Homo sapiens.
XX
PN   WO9807738-A1.
XX
PD   26-FEB-1998.
XX
PF   15-AUG-1997;   97WO-US15485.
XX
PR   19-AUG-1996;   96US-0023579.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Fujieda S,  Ke Z,  Saxon AW;
XX
DR   WPI; 1998-179050/16.
XX
PT   New immunoglobulin trans-spliced transcripts - used for, e.g.
PT   stimulating or inhibiting synthesis of particular immunoglobulin
PT   isotype, useful for treating immune disorders
XX
PS   Example 2; Page 36; 83pp; English.
XX
CC   The nucleotides AAV21362-V21373 are examples of the genomic fragments
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CC   from which sequences were used to create trans-spliced transcripts. The
CC   transcripts comprise a sequence capable of annealing to a human genomic
CC   immunoglobulin (Ig) heavy chain I region of a locus selected from mu,
CC   epsilon, alpha and gamma followed by a second sequence capable of
CC   annealing to a region of a second locus selected from mu, epsilon, alpha
CC   and gamma as above. The products can be used for stimulating or
CC   inhibiting synthesis of a particular human Ig isotype. They can be used
CC   for treating disorders mediated by IgM, IgG, IgA or IgE, in particular
CC   for inhibiting IgE synthesis or isotype switching to IgE for treating
CC   allergic disorders. They can also be used for treating autoimmune and
CC   alloimmune diseases amongst others.
XX
SQ   Sequence 60 BP; 9 A; 26 C; 12 G; 13 T; 0 other;


  Query Match             67.5%;  Score 16.2;  DB 19;  Length 60;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 ggctggtctgggatgtcggaa 22
           |||||||| ||||||  ||||
Db      45 GGCTGGTCGGGGATGCTGGAA 25


RESULT   4
AAT99618/c
ID   AAT99618 standard; DNA; 30 BP.
XX
AC   AAT99618;
XX
DT   06-JUL-1998  (first entry)
XX
DE   Protein kinase LIMK1 gene intron 10/exon 11 junction.
XX
KW   Williams syndrome cognitive profile; WSCP; cognition; LIM-kinase 1;
KW   LIMK1 gene; supra-vascular aortic stenosis; protein kinase; human;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   intron          1..20
FT                   /*tag= a
FT                   /note= "3' end of intron 10"
FT   exon            21..30
FT                   /*tag= b
FT                   /note= "5' end of exon 11"
XX
PN   WO9801740-A2.
XX
PD   15-JAN-1998.
XX
PF   07-JUL-1997;   97WO-US11687.
XX
PR   10-JUL-1996;   96US-0678039.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Morris CA;
XX
DR   WPI; 1998-101185/09.
XX
PT   Diagnosing Williams syndrome cognitive profile from hemizygosity of
PT   LIMK1 - gene on chromosome 7 encoding new kinase, allowing
PT   differentiation from classic Williams syndrome and supra-vascular
PT   aortic stenosis
XX
PS   Example 3; Page 24; 62pp; English.
XX
CC   This sequence comprises the junction between intron 10 and exon 11
CC   of the human LIM-kinase 1 (LIMK1) gene. Exon 11 contains 60
CC   nucleotides. The LIMK1 genomic structure was determined by DNA
CC   sequence analyses of genomic clones containing LIMK1. The gene
CC   consists of 16 exons (see also AAV05315 and AAT99599-T99629) and spans
CC   approximately 37 kb. The gene is located 15.4 kb 3' of the
CC   elastin gene in chromosome 7. It encodes a novel protein kinase
CC   (see AAW46576). A claimed method for determining the presence of
CC   Williams syndrome cognitive profile (WSCP) comprises determining
CC   the zygosity of the LIMK1 locus, with hemizygosity being indicative
CC   of impaired visuo-spatial constructive cognition. A claimed method
CC   for distinguishing whether an individual has Williams syndrome
CC   (WS), WSCP or SVAS (supra-vascular aortic stenosis) involves
CC   analysis of deletion of parts of chromosome 7. Deletion of the ELN
CC   (elastin) locus but not LIMK1 indicates SVAS, deletion of ELN and
CC   LIMK1 but no more than about 100 kb 3' to LIMK1 indicates WSCP, and
CC   deletion of ELN, LIMK1 and over 300 kb 3' of LIMK1 indicates WS.
XX
SQ   Sequence 30 BP; 6 A; 12 C; 4 G; 8 T; 0 other;


  Query Match             62.5%;  Score 15;  DB 19;  Length 30;
  Best Local Similarity   78.3%;  Pred. No. 6.9e+02;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 tggctggtctgggatgtcggaag 23
           ||||||  ||||||||  | |||
Db      28 TGGCTGTCCTGGGATGGAGAAAG 6


RESULT   5
AAT70675/c
ID   AAT70675 standard; RNA; 40 BP.
XX
AC   AAT70675;
XX
DT   29-JUL-1997  (first entry)
XX
DE   Fibrin clot binding ligand FCN8.
XX
KW   Ligand; peripheral blood mononuclear cell; fibrin clot; carotid artery;
KW   systematic evolution of ligands by exponential enrichment method; PBMC;
KW   epitope; macromolecule; tissue SELEX method; cancer screening; therapy;
KW   AIDS monitoring; localisation of thrombi; atherosclerosis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..40
FT                   /*tag= a
FT                   /mod_base= all C's are 2-fluorine-C
FT   modified_base   1..40
FT                   /*tag= b
FT                   /mod_base= all U's are 2-fluorine-U
XX
PN   WO9634874-A1.
XX
PD   07-NOV-1996.
XX
PF   01-MAY-1996;   96WO-US06059.
XX
PR   03-MAY-1995;   95US-0433126.
PR   03-MAY-1995;   95US-0433124.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
PA   (SCHD ) SCHERING AG.
XX
PI   Gold L,  Schneider DJ,  Speck U,  Stephens A;
XX
DR   WPI; 1996-506091/50.
XX
PT   Nucleic acid ligands used in cancer screening, AIDS monitoring etc.
PT   - bind to peripheral blood mononuclear cells, fibrin clots or
PT   carotid arteries
XX
PS   Claim 18; Page 51; 138pp; English.
XX
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CC   AAT70617-T70704 represent the random regions from a degenerate ssDNA
CC   library based on the sequence represented by AAT42819. These sequences
CC   are all ligands specific for fibrin clots identified using the method of
CC   the invention. The method of the invention is for identifying nucleic
CC   acid (NA) ligands and NA ligand sequences to a tissue target selected
CC   from peripheral blood mononuclear cells (PBMC's) (such as the ligands
CC   represented by AAT70584-T70616), fibrin clots (such as these sequences),
CC   and carotid arteries (such as the ligands represented by
CC   AAT70705-T70803). The method comprises preparing a candidate mixture of
CC   NA sequences, and contacting these with the tissue, whereby NAs having an
CC   increased affinity to the tissue relative to the candidate mixture may
CC   be partitioned from the remainder of the candidate mixture. The
CC   increased affinity NAs are then partitioned from the remainder of the
CC   candidate mixture, and are amplified to yield a mixture of NAs enriched
CC   for NA sequences with a relatively higher affinity and specificity for
CC   binding to the tissue, whereby NA ligands of the tissue may be
CC   identified. The method represents a tissue SELEX (systematic evolution of
CC   ligands by exponential enrichment) method.  The NA ligands and epitopes
CC   and macromolecules identified using the ligands can be used in diagnostic
CC   and therapeutic applications. In particular, they can be used for e.g.
CC   cancer screening, AIDS monitoring, detection and localisation of thrombi
CC   or atherosclerosis diagnosis and therapy.
XX
SQ   Sequence 40 BP; 14 A; 10 C; 11 G; 5 U; 0 other;


  Query Match             60.8%;  Score 14.6;  DB 17;  Length 40;
  Best Local Similarity   81.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tggctggtctgggatgtcgga 21
          | ||  ||||||||||| |||
Db     28 TAGCCCGTCTGGGATGTGGGA 8


RESULT   6
AAZ25247/c
ID   AAZ25247 standard; DNA; 33 BP.
XX
AC   AAZ25247;
XX
DT   15-DEC-1999  (first entry)
XX
DE   Plasmid construction PCR primer #3.
XX
KW   Apoptosis; regulation; chemically induced dimerisation; aggregation;
KW   artificial death switch; ADS; cysteine protease; caspase-1; ICE;
KW   caspase-3; YAMA; FK506-binding protein; FKBP; development;
KW   hyperproliferative disorder; tumour; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9950425-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06799.
XX
PR   30-MAR-1998;   98US-0079831.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Spencer DM,  Slawin KM;
XX
DR   WPI; 1999-591323/50.
XX
PT   Conditionally lethal artificial death switches based on chemically
PT   induced dimerisation of cysteine proteases  - useful for treating
PT   hyperproliferative diseases
XX
PS   Example 1; Page 20; 117pp; English.
XX
CC   The present invention describes a conditionally lethal molecule (A)
CC   comprising a chemical inducer binding domain and an apoptosis inducing
CC   factor, where the apoptosis inducing factor is an apoptosis signal
CC   transducing factor. A vector encoding (A) is useful for treating a
CC   disease, e.g. a hyperproliferative disease that is benign or malignant,
CC   or atherosclerosis. The nucleotide sequence (I) encoding (A) can be
CC   used to cause regression of a tumour, reduction in tumour size or
CC   reduction in PSA levels, by transfecting the nucleic acid into cells of
CC   the tumour. (I) can also be used to affect the rate of cell proliferation
CC   caused by BPH by transfecting (I) into prostate cells. (I) is also used
CC   to induce apoptosis in a cell as well as for determining the biological
CC   role of a cell type. The conditionally lethal gene is non-toxic unless
CC   induced. It does not require membrane localisation and bypasses
CC   endogenous apoptosis control mechanisms. The present sequence represents
CC   a PCR primer used in an example from the present invention.
XX
SQ   Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 other;


  Query Match             60.0%;  Score 14.4;  DB 20;  Length 33;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 tggctggtctgggatgtcggaagg 24
          ||  | ||||||||| |||| | ||
Db     32 TGCGTAGTCTGGGACGTCGTACGG 9


RESULT   7
AAZ25248
ID   AAZ25248 standard; DNA; 33 BP.
XX
AC   AAZ25248;
XX
DT   15-DEC-1999  (first entry)
XX
DE   Plasmid construction PCR primer #4.
XX
KW   Apoptosis; regulation; chemically induced dimerisation; aggregation;
KW   artificial death switch; ADS; cysteine protease; caspase-1; ICE;
KW   caspase-3; YAMA; FK506-binding protein; FKBP; development;
KW   hyperproliferative disorder; tumour; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9950425-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06799.
XX
PR   30-MAR-1998;   98US-0079831.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Spencer DM,  Slawin KM;
XX
DR   WPI; 1999-591323/50.
XX
PT   Conditionally lethal artificial death switches based on chemically
PT   induced dimerisation of cysteine proteases  - useful for treating
PT   hyperproliferative diseases
XX
PS   Example 1; Page 20; 117pp; English.
XX
CC   The present invention describes a conditionally lethal molecule (A)
CC   comprising a chemical inducer binding domain and an apoptosis inducing
CC   factor, where the apoptosis inducing factor is an apoptosis signal
CC   transducing factor. A vector encoding (A) is useful for treating a
CC   disease, e.g. a hyperproliferative disease that is benign or malignant,
CC   or atherosclerosis. The nucleotide sequence (I) encoding (A) can be
CC   used to cause regression of a tumour, reduction in tumour size or
CC   reduction in PSA levels, by transfecting the nucleic acid into cells of
CC   the tumour. (I) can also be used to affect the rate of cell proliferation
```

```
CC   caused by BPH by transfecting (I) into prostate cells. (I) is also used
CC   to induce apoptosis in a cell as well as for determining the biological
CC   role of a cell type. The conditionally lethal gene is non-toxic unless
CC   induced. It does not require membrane localisation and bypasses
CC   endogenous apoptosis control mechanisms. The present sequence represents
CC   a PCR primer used in an example from the present invention.
XX
SQ   Sequence 33 BP; 6 A; 6 C; 13 G; 8 T; 0 other;


  Query Match             60.0%;  Score 14.4;  DB 20;  Length 33;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 tggctggtctgggatgtcggaagg 24
          ||  | |||||||| |||| | ||
Db      6 tgcgtagtctgggacgtcgtacgg 29


RESULT   8
AAV00317/c
ID   AAV00317 standard; DNA; 43 BP.
XX
AC   AAV00317;
XX
DT   23-APR-1998  (first entry)
XX
DE   Bacillus thuringiensis insecticidal gene modification primer BTK31.
XX
KW   Insecticidal protein; Bacillus thuringiensis; monocotyledonous plant;
KW   structural gene; maize; CryI(b); CryIIB; primer; ss.
XX
OS   Synthetic.
OS   Bacillus thuringiensis.
XX
PN   US5689052-A.
XX
PD   18-NOV-1997.
XX
PF   19-SEP-1995;   95US-0530492.
XX
PR   22-DEC-1993;   93US-0172333.
PR   19-SEP-1995;   95US-0530492.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Brown SM,  Dean DA,  Fromm ME,  Sanders PR;
XX
DR   WPI; 1998-008070/01.
XX
PT   Genes encoding insecticidal proteins of Bacillus thuringiensis -
PT   modified to enhance expression in monocotyledonous plants
XX
PS   Example 1; Column 14; 86pp; English.
XX
CC   The present sequence represents a primer used in the present invention
CC   describing new structural genes capable of being expressed in a
CC   monocotyledonous plant. The new genes comprise modified nucleotide
CC   sequences which encode insecticidal proteins of Bacillus thuringiensis.
CC   The genes have been modified to reduce the usage of codons that are
CC   rare or semi-rare in monocotyledon DNA, thereby increasing
CC   transformation efficiency and/or increasing accumulation of the
CC   insecticidal protein in monocotyledon tissues.
XX
SQ   Sequence 43 BP; 11 A; 21 C; 2 G; 9 T; 0 other;


  Query Match             60.0%;  Score 14.4;  DB 19;  Length 43;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 tggctggtctgggatgtcggaagg 24
          ||| || | ||||| | ||||| |
Db     25 TGGGTGATTTGGGAGGACGGAATG 2


RESULT   9
AAF73235/c
ID   AAF73235 standard; DNA; 43 BP.
XX
AC   AAF73235;
XX
DT   26-APR-2001  (first entry)
XX
DE   Oligonucleotide #26.
XX
KW   CryIA; transgenic; crystal; toxin; insecticide; ss.
XX
OS   Synthetic.
XX
PN   US6180774-B1.
XX
PD   30-JAN-2001.
XX
PF   05-AUG-1997;   97US-0906517.
XX
PR   19-SEP-1995;   95US-0530492.
PR   22-DEC-1993;   93US-0172333.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Brown SM,  Dean DA,  Fromm ME,  Sanders PR;
XX
DR   WPI; 2001-190861/19.
XX
PT   Novel nucleic acids, useful for transgenic plant production which is
PT   capable of expressing increased levels of desired proteins -
XX
PS   Example 1; Column 14; 81pp; English.
XX
CC   The present invention relates to nucleotides 669-1348 of a
CC   B.thuringiensis CryIA(b). The invention is useful for transgenic
CC   plant production, e.g. maize, capable of expressing increased
CC   amount of transgenic protein, e.g. crystal protein toxin gene
CC   of Bacillus thuringiensis.
XX
SQ   Sequence 43 BP; 11 A; 21 C; 2 G; 9 T; 0 other;


  Query Match             60.0%;  Score 14.4;  DB 22;  Length 43;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 tggctggtctgggatgtcggaagg 24
          ||| || | ||||| | ||||| |
Db     25 TGGGTGATTTGGGAGGACGGAATG 2


RESULT  10
AAZ49486/c
ID   AAZ49486 standard; DNA; 31 BP.
XX
AC   AAZ49486;
XX
DT   04-APR-2000  (first entry)
XX
DE   PCR primer XDH2UP-S1 for amplifying Gluconobacter XDH gene.
XX
KW   PCR primer; XDH; Xylitol dehydrogenase; xylitol; low calorie sweetener;
KW   dental caries; fluid therapy; diabetes mellitus; ss.
XX
OS   Gluconobacter oxydans.
XX
PN   EP976827-A1.
XX
PD   02-FEB-2000.
```

XX
PF 30-JUL-1999; 99EP-0114971.
XX
PR 30-JUL-1998; 98JP-0216047.
XX
PA (AJIN) AJINOMOTO KK.
XX
PI Sugiyama M, Tonouchi N, Suzuki S, Yokozeki K;
XX
DR WPI; 2000-118551/11.
XX
PT New proteins for production of xylitol, useful as food sweetener and
PT for treatment of diabetes mellitus -
XX
PS Example 3; Page 24; 31pp; English.
XX
CC The present sequence is PCR primer XDH2UP-S1. This was used in the
CC preparation of DNA fragment of upstream region of XDH2 (xylitol
CC dehydrogenase) by using TakaRa LA PCR in vitro Cloning Kit. The PCR
CC reaction was performed by using Gene Amp PCR System 9600. XDH acts upon
CC D-xylulose to produce xylitol which is used as a low calorie sweetener
CC and prevents dental caries. Xylitol is also useful for fluid therapy in
CC the treatment of diabetes mellitus.
XX
SQ Sequence 31 BP; 6 A; 12 C; 7 G; 6 T; 0 other;

Query Match 59.2%; Score 14.2; DB 21; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 tggtctgggatgtcggaag 23
|||||| |||| |||||||
Db 22 TGGTCCGGGACTTCGGAAG 4

RESULT 11
AAQ49692/c
ID AAQ49692 standard; DNA; 20 BP.
XX
AC AAQ49692;
XX
DT 25-APR-1994 (first entry)
XX
DE PKC-gamma translation initiation codon binding oligomer 215-196.
XX
KW Antisense; oligonucleotide; inter-sugar linkage; protein kinase C;
KW phosphorothionate linkage; PKC; transcription initiation site;
KW translation initiation site; 5' cap region; intron/exon boundary;
KW diagnosis; therapeutics; prophylaxis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "Phosphorothionate linkages"
XX
PN WO9319203-A.
XX
PD 30-SEP-1993.
XX
PF 25-FEB-1993; 93WO-US02213.
XX
PR 16-MAR-1992; 92US-0852852.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean N;
XX
DR WPI; 1993-320768/40.
XX
PT Oligo-nucleotide(s) hybridise to nucleic acids encoding Protein
PT kinase C - useful as diagnostics and therapeutics for disease
PT states associated with particular isozymes of PKC
XX
PS Claim 6; Page 19; 64pp; English.
XX
CC The sequences given in AAQ49657-707 are antisense oligonucleotides
CC which contain altered inter-sugar linkages, pref. phosphorothionate
CC linkages. These oligomers bind with the protein kinase C (PKC) mRNA
CC at the transcription initiation site, the translation initiation
CC site, the 5' cap region, an intron/exon boundary, coding sequences
CC or sequences in the 5'- or 3'-untranslated regions. These
CC oligonucleotides may be used in diagnostics, therapeutics,
CC prophylaxis and as research reagents. The numbers allocated to
CC the oligonucleotides are relative to the first residue to be sequenced
CC on the cDNA, which is 28 residues upstream of the ATG start codon.
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match 58.3%; Score 14; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggctggtctggga 14
|||||||||||||||
Db 19 TGGCTGGTCTGGGA 6

RESULT 12
AAQ97909/c
ID AAQ97909 standard; DNA; 20 BP.
XX
AC AAQ97909;
XX
DT 17-OCT-1995 (first entry)
XX
DE PNA oligomer targetting AUG region of PKC-tau.
XX
KW Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;
KW cell proliferation; cell differentiation; isozyme; antisense;
KW triple helix; cancer; psoriasis; inflammation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "at least one (and preferably all) of
FT the backbone subunits are composed of N-acetyl
FT N-(2-aminoethyl)glycine peptide residues, the
FT nucleobase being attached covalently to the
FT acetyl group and the peptide linkage being
FT formed by condensation of the glycine
FT carboxy group of one residue with the amino
FT group of the 2-aminoethyl moiety in the next
FT residue"
XX
PN WO9503833-A.
XX
PD 09-FEB-1995.
XX
PF 28-JUL-1994; 94WO-US08465.
XX
PR 29-JUL-1993; 93US-0099098.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM;
XX
DR WPI; 1995-082040/11.
XX
PT New peptide nucleic acid oligomers specific for protein kinase C
PT isozyme(s) - useful as anti:sense molecules for treating PKC

PT mediated disease, e.g. cancer, psoriasis and inflammation
XX
PS Claim 17; Page 264; 287pp; English.
XX
CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC of naturally occurring nucleobases covalently bound to a polyamide
CC backbone and (b) hybridise to the translation initiation AUG region,
CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region
CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target
CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene
CC regulation moieties. They inhibit expression of PKC-alpha and its
CC isoforms (including beta, gamma, delta, epsilon, zeta and eta) and so
CC are useful for treating and diagnosing cell proliferation and
CC differentation processes such as neoplastic, hyperproliferative
CC and inflammatory diseases.
CC PNA oligomers have high affinity for complementary single stranded DNA.
CC They are also able to form triple helices in which a first PNA strand
CC binds with RNA or ssDNA and a second PNA strand binds with the resulting
CC double helix or with the first PNA strand. The PNAs possess no
CC significant charge and are water soluble, which facilitates cellular
CC uptake. Futher, since they contain amides of non-biological amino acids,
CC they are biostable and resistant to enzymatic degradation by proteases.
CC The present sequence targets the AUG region of PKC-tau.
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match 58.3%; Score 14; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggctggtctggga 14
||||||||||||||
Db 19 TGGCTGGTCTGGGA 6

RESULT 13
AAQ84196/c
ID AAQ84196 standard; DNA; 20 BP.
XX
AC AAQ84196;
XX
DT 21-SEP-1995 (first entry)
XX
DE PKC-gamma antisense oligo, binds to cDNA bases 196-215.
XX
KW Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon;
KW zeta; modulation; expression; isozyme; hybridise; 5' UTR; human;
KW 3' untranslated region; translation initiation site; detection;
KW phosphorothioate linkage; 2'-O-methyl modification;
KW 2'-O-propyl modification; ss.
XX
OS Synthetic.
XX
PN WO9502069-A.
XX
PD 19-JAN-1995.
XX
PF 08-JUL-1994; 94WO-US07770.
XX
PR 09-JUL-1993; 93US-0089996.
PR 22-FEB-1994; 94US-0199779.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Boggs RT, Dean NM;
XX
DR WPI; 1995-066911/09.
XX
PT Oligo:nucleotide(s) hybridisable with Protein Kinase C mRNA or
PT gene - also novel PKC-alpha 3'-UTR sequence, useful for
PT diagnosis and treatment of hyperproliferative disorders.
XX
PS Claim 15; Page 27; 125pp; English.
XX
CC The sequences given in AAQ84195-99 are oligos which are antisense to
CC the protein kinase C-gamma (PKC-gamma) cDNA. These oligos are anti-
CC sense to regions in the 5' untranslated region of the cDNA and around
CC the translation initiation site. These antisense molecules may be
CC used in modulating the expression of this particular isozyme of PKC.
CC The oligos of the invention preferably hybridise with the 5'- or 3'-
CC untranslated regions of the PKC gene, or the translation initiation
CC site, or the coding region. These oligos may be used in the detection
CC of the human PKC genes and for treatment of animals with conditions
CC associated with PKC, esp. hyperproliferative diseases such as psoriasis,
CC colorectal cancer, lung cancer, breast or skin cancer. These oligos may
CC contain at least one phosphorothioate linkage and/or at least one of the
CC nucleotides comprises a modification on the 2' position of the sugar,
CC esp. a 2'-O-methyl or a 2'-O-propyl modification.
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match 58.3%; Score 14; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggctggtctggga 14
||||||||||||||
Db 19 TGGCTGGTCTGGGA 6

RESULT 14
AAV35536/c
ID AAV35536 standard; DNA; 20 BP.
XX
AC AAV35536;
XX
DT 01-SEP-1998 (first entry)
XX
DE Oligo ON36 targeted to human protein kinase C (PKC)-gamma.
XX
KW Protein kinase C; PKC; target; hybridisation; human; liposome;
KW sterically stabilised; neoplastic disorder; inflammatory disorder;
KW hyperproliferative disorder; cancer; psoriasis; PKC-gamma; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9809633-A2.
XX
PD 12-MAR-1998.
XX
PF 03-SEP-1997; 97WO-EP04796.
XX
PR 04-SEP-1996; 96GB-0018376.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Hamilton KO, Love WG, Nicklin PL, Phillips JA;
XX
DR WPI; 1998-260955/23.
XX
PT Oligo:nucleotide compositions for protein kinase C disorders -
PT comprising sequence hybridisable to protein kinase C gene entrapped
PT in sterically stabilised liposomes
XX
PS Claim 21; Page 8; 25pp; English.
XX
CC This represents an oligonucleotide sequence that is specifically
CC hybridisable with DNA or RNA derived from a protein kinase C (PKC) gene,
CC entrapped in sterically stabilised liposomes. Compositions comprising
CC such oligonucleotides can be used in the treatment of PKC disorders and
CC for modulating the expression of PKC in cells. They can be used in the
CC diagnosis and treatment of disorders associated with PKC, particularly
CC neoplastic, inflammatory and hyperproliferative disorders such as cancer

CC or psoriasis. The compositions retain high activity after prolonged
CC circulation in the bloodstream and exhibit reduced accumulation of
CC oligonucleotides in non-target organs such as the liver and kidney.
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match 58.3%; Score 14; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggctggtctggga 14
||||||||||||||
Db 19 TGGCTGGTCTGGGA 6

RESULT 15
AAZ27301/c
ID AAZ27301 standard; DNA; 20 BP.
XX
AC AAZ27301;
XX
DT 01-DEC-1999 (first entry)
XX
DE Human protein kinase C gamma antisense oligonucleotide #2.
XX
KW Human; protein kinase C; PKC; diagnosis; antisense oligonucleotide;
KW phosphorothioate; hybridisation; isozyme; target; inflammation;
KW hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5959096-A.
XX
PD 28-SEP-1999.
XX
PF 07-JUN-1995; 95US-0481066.
XX
PR 16-MAR-1992; 92US-0852852.
PR 09-JUL-1993; 93US-0089996.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean N;
XX
DR WPI; 1999-561076/47.
XX
PT Antisense oligonucleotides useful for treatment of hyperproliferative
PT and inflammatory conditions including psoriasis, tumours and cancer -
XX
PS Claim 1; Column 16; 56pp; English.
XX
CC The present invention describes antisense oligonucleotides up to 50
CC nucleotides in length which specifically bind mRNA encoding human
CC protein kinase C (PKC). AAZ27266 to AAZ27386 represent human PKC
CC antisense oligonucleotides used in the exemplification of the present
CC invention. The antisense oligonucleotides are useful for the treatment of
CC diseases associated with PKC expression, such as hyperproliferative and
CC inflammatory conditions including psoriasis, tumours and cancer
CC (glioblastoma, bladder, breast, colon and lung cancer).
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match 58.3%; Score 14; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggctggtctggga 14
||||||||||||||
Db 19 TGGCTGGTCTGGGA 6

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